protein or a functional subsequence thereof is fused with another protein, such as β-galactosidase, glutathione-S-transferase, protein A *etc.* In the context of fusion proteins, see *e.g.* Smith and Johnson (1988) *Gene* 67:31; Hopp *et al.* (1988) *Biotechnology* 6:1204; La Vallie *et al.* (1993) *Biotechnology* 11:187.--

Replace the paragraph beginning at page 22, line 1, with the following rewritten paragraph:

--Competitive assay formats are preferred in the present context, wherein the amount of analyte, preferably an unknown quantity of antibodies in a subject, in a sample is measured indirectly by measuring the amount of added analyte, displaced from a capture agent by the analyte present in the sample. Most preferred are the enzyme-linked immunosorbent assay (ELISA) methods, in which an antibody typically is bound to an enzyme, such as peroxidase or phosphatase, which can produce colored reaction products from an appropriate buffer. Thus, it utilizes a tagged antigen molecule of known quantity to determine an unlabelled antigen of unknown quantity. Preferably, the protein according to the invention, or a suitable functional fragment thereof, is used coupled to a conventional tag, such as His6(Piece of SEQ ID NO: 3). This assay is *e.g.* useful to diagnose *Sarcoptes scabiei* infection in dogs.--

Replace the paragraph beginning at page 27, line 4, with the following rewritten paragraph:

--Cloning of part of the 5' cDNA end of MSA1

A PCR strategy was used in order to clone regions upstream of the cDNA insert in pPU3. In the first PCR the primer KBE 5 (5'CAC TAT CGG AGA ACG TAA CTT CGG 3') (SEQ ID NO: 4), complementary to the anti-sense strand of the insert in pPU3, was desigend and used together with a T3 primer, complementary to the vector used to construct the cDNA library. As a template the *S. scabiei* cDNA-libray was used. The resulting fragment was cloned into the *Sma*I-site of pUC18 and sequenced as above. This new fragment was then used for the design of a second primer KBE 8 (5'CCT GGC ATT CTA CTT GAG ATG TA 3') (SEQ ID NO: 5) for the amplification an additional 5'end cDNA fragment. The second 5'end fragment was cloned and sequenced as above. A continuos cDNA which included the original MSA1 cDNA and both of the 5' end fragments was generated by using the Titan™ One Tube RT-PCR system (manufactured by Roche). For the reverse transriptase step the reverse primer MSA1Xba (5'CGC **TCT AGA** CTC AAC AAT GAA TGT CTG CAA 3') (SEQ ID NO: 6) was used. In the PCR, the reverse primer was used in combination with the forward primer LDL 2 (5'CG**G GAT CC**G AAT ATT TCG TCT CGA AAC CG 3') (SEQ ID NO: 7). The resulting fragment was cloned into the *Bam*HI-*Xba*I sites of pPU16 utilizing the recognition sites introduced during the PCR (shown in boldface). A graphic overview of the cloning strategy is shown in Fig.--

Attached hereto is a marked-up version of the changes made to the specification. The attached page is captioned "VERSION WITH MARKINGS TO SHOW CHANGES MADE."

Respectfully submitted,

YOUNG & THOMPSON

By _____

Robert J. Patch
Attorney for Applicant
Registration No. 17,355
745 South 23rd Street
Arlington, VA 22202
Telephone: 521-2297

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